Qtl Mapping of Pathogenicity in *Heterobasidion annosum sensu lato*

Åke Olson; Mårten Lind; Jan Stenlid

Department of Forest Mycology and Pathology, Swedish University of Agricultural Sciences. Box 7026, S-750 07 Uppsala, Sweden
ake.olson@mykopat.slu.se

Heterobasidion annosum (Fr.) Bref. s*ensu lato*, casual agent of annosum root rot in conifers, is the economical most devastating forest pathogen in the northern hemisphere. A genetic linkage map of *H. annosum*, was constructed from a compatible mating between isolates from the North American S and P intersterility groups. The linkage analysis of 358 AFLP markers in 102 progeny isolates generated 19 linkage groups containing 6 or more markers that covered 1468 cM.

Two distinct methods were used to analyse the segregation of pathogenicity. 1 year old pine seedlings grown in the greenhouse were infected with *H. annosum* progeny isolates. Pathogenicity was measured as mean necrosis lengths caused in 10 pine plants. One QTL for pathogenicity was found on linkage group 15 with a LOD peak of 2.95, spanning a 31.2 cM large area. This QTL explained 14.3% of the variation. Another QTL were found in a small linkage group containing 5 markers and spanning 36.8 cM, with a LOD peak of 4.40 at marker *paacts02*. 19.1% of the variation could be explained by this QTL. The heritability of pathogenicity on pine was estimated to be 0.21 in this study.

The disease increase rate values from an *in vitro* test were used as another estimate of pathogenicity and used for the QTL-analysis. From the *in vitro* pathogenicity test, a large area of 26.5 cM on linkage group 11 between the markers *acgcs5* and *paacgp08* contains a high QTL probability of LOD 3.09. This QTL explained 16.4% of the total variation in this experiment. The heritability of pathogenicity on pine was estimated to be 0.088 in this study.

Successfully localization of the two intersterility genes (S and P) on the map were carried out through mating of the progeny isolates with three tester strains carrying known intersterility genotypes.

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